

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on:

February 21, 2003, 12:30:13 ; Search time 92 Seconds

(without alignments)

4.479 Million cell updates/sec

Title: SHORT-PEP  
Perfect score: 16  
Sequence: 1 rw 2

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : SPTRMBL21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mic:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rabbit:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriaph:  
17: sp\_archeap:  
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result NO.	Score	Query Length	DB ID	Description
1	6	37.5	5 13	P83308 gallus galli
2	12.5	4 11	008433	P83308 gallus galli
3	12.5	5 2	P83073	P83073 bacillus ce
4	12.5	5 10	099007	Q99007 hordeum vul

## ALIGNMENTS

RESULT 1	P83308	PRELIMINARY;	PRT;	5 AA.
ID P83308				
AC P83308;				
DT 01-JUN-2002 (TREMBREL. 21, Created)				
DT 01-JUN-2002 (TREMBREL. 21, Last sequence update)				
DT 01-JUN-2002 (TREMBREL. 21, Last annotation update)				

DE FMRFamide-like neuropeptide (IPLRF-amide).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galiformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=BRAIN;  
RX PubMed=613771;  
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
RT "A novel active pentapeptide from chicken brain identified by  
antibodies to FMRFamide.";  
RL Nature 305:328-330(1983).  
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 645 MW; 69Da073767400000 CRC64;  
Query Match 37.5%; Score 6; DB 13; Length 5;  
Best Local Similarity 50.0%; Pred. No. 6.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RW 2  
Db 4 RF 5

RESULT 2  
008433 PRELIMINARY; PRT; 4 AA.  
ID 008433  
AC Q08433;  
DT 01-NOV-1996 (TREMBREL. 01, Created)  
DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)  
DT 01-JAN-1999 (TREMBREL. 09, Last annotation update)  
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)  
DE (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GUNN;  
RX MEDLINE=9128275B; PubMed=1840486;  
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;  
RT hyperbilirubinemic Gunn rat.";  
RL Blochem. Biophys. Res. Commun. 177:1161-1164(1991).  
CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPATOR  
CC BETA-D-GLUCURONOSIDE.  
CC -!- SUBCELLULAR LOCATION: MICROSOME.  
DR EMBL; S88636; ABAB1929; 1;  
KW Transferase; Glycosyltransferase; Microsome; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 4  
FT NON\_TER 4  
SQ SEQUENCE 4 AA; 473 MW; 633732C20000000 CRC64;  
Query Match 12.5%; Score 2; DB 11; Length 4;  
Best Local Similarity 0.0%; Pred. No. 6.7e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
P83073

PRELIMINARY; PRT; 5 AA.

P83073; PRELIMINARY; PRT; 5 AA.

AC P83073;

DT 01-OCT-2001 (TREMBREL\_18, Created)

DT 01-OCT-2001 (TREMBREL\_18, Last sequence update)

DT 01-OCT-2001 (TREMBREL\_18, Last annotation update)

DE 88 kDa protein (Fragment).

OS Bacillus cereus.

OC Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

NCBI\_TaxID=1396;

RN [1]

RP SEQUENCE.

RC STRAIN=NCTMB 11796;

RA Brownie N.; Dowds B.C.A.;

RL Submitted (JUL-2001) to the SWISS-PROT data bank.

FT NON\_TER 5

SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336P00000 CRC64;

Query	Match	12.5%	Score	2	DB	2	Length	5
	Best local similarity	0.0%	Pred. No.	6.7e-05				
Qy	Matches	0	Conservative	1	Mismatches	0	Indels	0
Db	Gaps	0						0
Db	K	2						
Db	;							

RESULT 4

Q99007 PRELIMINARY; PRT; 5 AA.

ID Q99007; PRELIMINARY; PRT; 5 AA.

AC Q99007;

DT 01-NOV-1996 (TREMBREL\_01, Created)

DT 01-NOV-1996 (TREMBREL\_01, Last sequence update)

DT 01-NOV-1998 (TREMBREL\_08, Last annotation update)

DE Alpha-amylase (EC 3.2.1.1) (Fragment).

GN AMY1.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

OC NCBL\_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;

RX MEDLINE=91329704; PubMed=183105;

RA Jacobsen J.V.; Close T.J.;

RT "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers.", Plant Mol. Biol., 16:713-721(1991).

RT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

RT Plant Mol. Biol., 16:713-721(1991).

CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

CC -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.

CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.

DR EMBL: X34643; CAA38455; 1; -.

KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination; Calcium; Multigene family.

FT NON\_TER 5

SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query	Match	12.5%	Score	2	DB	10	Length	5
	Best local similarity	0.0%	Pred. No.	6.7e-05				
Qy	Matches	0	Conservative	1	Mismatches	0	Indels	0
Db	Gaps	0						0
Db	K	4						
Db	;							

Query Match 12.5%; Score 2; DB 10; Length 5;  
 Best local similarity 0.0%; Pred. No. 6.7e-05; DB 10;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0;  
 Gaps 0;

Search completed: February 21, 2003, 12:33:48  
 Job time : 93 secs